



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/050,692 B

Source:

IFW16

Date Processed by STIC:

7/13/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby,
Room 1B03, Arlington, VA 22202

Revised 05/17/04



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/050,692B

DATE: 07/13/2004

TIME: 11:43:56

Input Set : A:\30331002-004.txt

Output Set: N:\CRF4\07132004\J050692B.raw

4 <110> APPLICANT: Carney, Darrell H.
 5 Crowther, Roger S.
 6 Simmons, David J.
 7 Yang, Jinping
 8 Redin, William R.
 10 <120> TITLE OF INVENTION: Stimulation of Bone Growth with Thrombin
 11 Peptide Derivatives
 13 <130> FILE REFERENCE: 3033.1002-004
 15 <140> CURRENT APPLICATION NUMBER: US 10/050,692B
 16 <141> CURRENT FILING DATE: 2002-01-16
 18 <150> PRIOR APPLICATION NUMBER: US 09/909,122
 19 <151> PRIOR FILING DATE: 2001-07-19
 21 <150> PRIOR APPLICATION NUMBER: US 60/219,300
 22 <151> PRIOR FILING DATE: 2000-07-19
 E--> 24 <160> NUMBER OF SEQ ID NOS: 6 - Found 7
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0

**Does Not Comply
 Corrected Diskette Needed**

(pg. 1-2)

ERRORED SEQUENCES

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/050,692B

DATE: 07/13/2004

TIME: 11:43:57

Input Set : A:\30331002-004.txt

Output Set: N:\CRF4\07132004\J050692B.raw

L:51 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:55 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
 L:60 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
 L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
 L:86 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:90 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
 L:94 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
 L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
 L:122 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
 L:143 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
 L:147 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
 L:24 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6) Counted (7)

↑

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.